



IFW16

RAW SEQUENCE LISTING

DATE: 07/27/2004

PATENT APPLICATION: US/09/292,053A

TIME: 15:35:33

Input Set : A:\37003-275739.APP.txt

Output Set: N:\CRF4\07272004\I292053A.raw

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3 <110> APPLICANT: REFF, MITCHELL E.
4     KLOETZER, WILLIAM S.
5     NAKAMURA, TAKEHIKO
7 <120> TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
8     THEREOF AS THERAPEUTICS
10 <130> FILE REFERENCE: 037003-0275739
12 <140> CURRENT APPLICATION NUMBER: 09/292,053A
13 <141> CURRENT FILING DATE: 1999-04-14
15 <150> PRIOR APPLICATION NUMBER: 08/803,085
16 <151> PRIOR FILING DATE: 1997-02-20
18 <160> NUMBER OF SEQ ID NOS: 39
20 <170> SOFTWARE: PatentIn Ver. 2.1
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23 <211> LENGTH: 390
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
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31 <220> FEATURE:
32 <221> NAME/KEY: mat_peptide
33 <222> LOCATION: (58)..(390)
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37 <222> LOCATION: (1)..(390)
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41 Met Ala Trp Thr Leu Leu Leu Val Thr Leu Leu Thr Gln Gly Thr Gly
42 -15 -10 -5
44 tcc tgg gct cag tct gcc ccg act cag cct tct gtg tct ggg tct 96
45 Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser
46 -1 1 5 10
48 cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt 144
49 Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
50 15 20 25
52 ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc 192
53 Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
54 30 35 40 45
56 ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct 240
57 Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
58 50 55 60
60 gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 288
61 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile

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64 tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat 336
65 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
66          80          85          90
68 aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc 384
69 Thr Thr Ser Ser Thr Leu Leu Phe Gly Arg Gly Thr Arg Leu Thr Val
70          95          100          105
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73 Leu Gly
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87 <221> NAME/KEY: mat_peptide
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92 <222> LOCATION: (1)..(423)
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96 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
97          -15          -10          -5
99 gtc ctg tcc cag ctg cag ctg cag gag tgc ggc cca gga gtg gtg aag 96
100 Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
101          -1 1 5 10
103 cct tgc gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc 144
104 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
105          15          20          25
107 agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga 192
108 Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
109 30          35          40          45
111 ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac 240
112 Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
113          50          55          60
115 aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag 288
116 Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
117          65          70          75
119 aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc 336
120 Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
121          80          85          90
123 gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta 384
124 Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
125          95          100          105
127 ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 423

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142 <221> NAME/KEY: mat_peptide
143 <222> LOCATION: (67)..(387)
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(387)
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152      -20                      -15                      -10
154 ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96
155 Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
156      -5                      -1    1                      5                      10
158 ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144
159 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
160      15                      20                      25
162 cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192
163 Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
164      30                      35                      40
166 gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240
167 Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
168      45                      50                      55
170 cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288
171 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
172      60                      65                      70
174 gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336
175 Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
176 75                      80                      85                      90
178 gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc 384
179 Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
180      95                      100                      105
182 aaa 387
183 Lys
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189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <221> NAME/KEY: sig_peptide
193 <222> LOCATION: (1)..(58)

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196 <221> NAME/KEY: mat_peptide
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206 -15 -10 -5
208 gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag 96
209 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
210 -1 1 5 10
212 cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc 144
213 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
214 15 20 25
216 acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag 192
217 Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
218 30 35 40 45
220 ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg 240
221 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
222 50 55 60
224 tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc 288
225 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
226 65 70 75
228 aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg 336
229 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
230 80 85 90
232 gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc 384
233 Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
234 95 100 105
236 cag gga gtc ctg gtc acc gtc tcc tca 411
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238 110 115
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255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
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259 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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292 <213> ORGANISM: Artificial Sequence
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302 <211> LENGTH: 34
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304 <213> ORGANISM: Artificial Sequence
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313 <210> SEQ ID NO: 11
314 <211> LENGTH: 34
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
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327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
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331 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
333 <400> SEQUENCE: 12
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VERIFICATION SUMMARY

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